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10/087,035	02/27/2002	Robert Kincaid	1001011076-1	6480

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EXAMINER	
SMITH, CAROLYN L	
ART UNIT	PAPER NUMBER
1631	

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Please find below and/or attached an Office communication concerning this application or proceeding.

The time period for reply, if any, is set in the attached communication.

Office Action Summary	Application No.	Applicant(s)	
	10/087,035	KINCAID, ROBERT	
	Examiner	Art Unit	
	Carolyn L. Smith	1631	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE *3* MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *16 May 2008*.

2a)☒ This action is **FINAL**. 2b)☐ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *1-11,22,27,28,31-37,41-44 and 47-49* is/are pending in the application.

4a) Of the above claim(s) _____ is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *1-11, 22, 27-28, 31-37, 41-44, and 47-49* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☐ The specification is objected to by the Examiner.

10)☐ The drawing(s) filed on _____ is/are: a)☐ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☐ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☐ Information Disclosure Statement(s) (PTO/SB/08) Paper No(s)/Mail Date _____.
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____ .
5) ☐ Notice of Informal Patent Application
6) ☐ Other: _____.

DETAILED ACTION

Applicant's amendments and remarks, filed 5/16/08, are acknowledged. Amended claims 1, 2, 5, 6, 7, 10, 11, 22, 27, 28, 31-37, 41-44, 47-49 and cancelled claims 12-21, 23-26, 29-30, 38-40, 45-46 are acknowledged.

Applicant's arguments, filed 5/16/08, have been fully considered but they are not deemed to be persuasive. Rejections and/or objections not reiterated from the previous office actions are hereby withdrawn. The following rejections and/or objections are either reiterated or newly applied. They constitute the complete set presently being applied to the instant application.

Claims 1-11, 22, 27-28, 31-37, 41-44, and 47-49 are herein under examination.

Claim Rejections – 35 USC § 103

The following is a quotation of 35 U.S.C. 103(a) which forms the basis for all obviousness rejections set forth in this Office action:

(a) A patent may not be obtained though the invention is not identically disclosed or described as set forth in section 102 of this title, if the differences between the subject matter sought to be patented and the prior art are such that the subject matter as a whole would have been obvious at the time the invention was made to a person having ordinary skill in the art to which said subject matter pertains. Patentability shall not be negatived by the manner in which the invention was made.

Claims 1-11, 22, 27-28, 31-37, 41-44, and 47-49 are rejected under 35 U.S.C. 103(a) as being unpatentable over Zhou et al. (US 2003/0120432 A1) further in view of Markowitz et al. (US 2003/0100999) and Cracauer et al. (US 20070178474).

The priority date relied upon for US 2003/0120432 A1 and 2007/0178474 A1 and comes from provisional applications.

This rejection is maintained and reiterated for reasons of record.

Copies of the provisional applications are not included with this Office action, because the copies could not be readily obtained when the Office action was mailed. Should applicant desire a copy of such a provisional application, applicant should promptly request the copy from the Office of Public Records (OPR) in accordance with 37 CFR 1.14(a)(1)(iv), paying the required fee under 37 CFR 1.19(b)(1). If a copy is ordered from OPR, the shortened statutory period for reply to this Office action will not be reset under MPEP § 710.06 unless applicant can demonstrate a substantial delay by the Office in fulfilling the order for the copy of the provisional application. Where the applicant has been notified on the PTO-892 that a copy of the provisional application is not readily available, the provision of MPEP § 707.05(a) that a copy of the cited reference will be automatically furnished without charge does not apply.

Zhou et al. describe a method for generating a custom probe array design wherein a system receives user-selected identifiers (array design parameters) (abstract), as stated in instant claims 1, 6, 22. Zhou et al. describe the user selecting probe set identifiers from a corresponding list that correspond to a gene (paragraph 0009). Zhou et al. describe a web portal processes inquiries regarding biological information for microarray experiments and a user selects « probe set identifiers » which enable detection of nucleic acids and corresponding genes which are identified (paragraphs 0005, 0009), as user requesting a corresponding probe set for a specified gene sequence (0093), and receiving one or more genes from a user as well as user notations (0168 and 0169) which represents receiving from a customer, at least one array design parameter

and notification of at least one gene of interest, as stated in instant claims 1, 22, 27. Zhou et al. describe accessing databases to provide researchers with associations between probe sets and gene identifiers, using Entrez search and retrieval system that provides information from various NCBI databases including nucleotide sequences, including accessing NCBI Entrez nucleotide database, and associations of a gene or probe-set identifier to products and a genomics database (0075, 0076, 0084, 0033, 0027, 0028, 0034), a user requesting a corresponding probe set for a specified gene sequence, and a database with the sequence or sequences from which the probes are designed (0093), and accessing/searching a database to obtain sequence data for probe selection for at least one gene of interest such that the correspondence may be provided to the user (0095, 0096, 0124, 0110, 0112, 0116, 0119, 0122), searching database for user provided sequence to verify existence of one or more corresponding probe sets and correlating identity of probe sets having a corresponding sequence with probe set identifiers (0124), or analyzing user provided input sequence to determine which portions should be represented by probes (0125), and databases including information relating probe set identifiers to probe sequences (0114) which represents database searching to obtain sequence data for probe selection for at least one gene of interest, as stated in instant claims 1, 22, 27. Zhou et al. describe analyzing a sequence to determine which portions of the sequence should be represented by probes which does not include short, common repeats because they are ineffective in uniquely representing the sequence (0125). Zhou et al. describe the verifier/designer applies various criteria and tests to verify and selects or designs probe sequences appropriate for representing the user-provided sequence (0125, 0140), as stated in instant claims 1, 22, 27. Zhou et al. describe the user may select many probe array format factors such as number of probes, dimensions of probes,

maximum number of probes representing one or more genes, substrate material that are received from the user (0009, 0138, 0140) which represents providing/receiving other selected array design parameters from the customer, as stated in instant claim 1. Zhou et al. describe a probe array generator that generates a custom probe array design from the associated probe sets and probe array format information (0142) and synthesizes the probe arrays (0010) which represents completing the array design and fabricating the array, as stated in instant claims 1, 22, 27, 28. Zhou et al. describe the genomic portal system receives user-selected identifiers including sequence information, the system verifies probes corresponding to identifiers and generates a custom probe array design (paragraphs 0006 and 0008) and constructing and arranging arrays to detect and/or measure any one gene expression (paragraph 0007). Zhou et al. describe using remote vendor business systems and servers (Figure 4, #404 and paragraph 0134) and the user data processor then receiving the custom probe array design, as stated in instant claims 1, 2, 22, 27, 31. Zhou et al. describe further generation including modifying or rejecting one or more user-selected probe array format factors including user-selected probe set identifiers and displaying this information to the user (paragraph 0010) which represents the vendor selecting at least one probe specific for the gene sequence, as stated in instant claims 1, 22, 27. Zhou et al. describe a verifier/designer performs an analysis of the user-provided input sequence to determine which portions of the sequence should be represented by probes because some portions may consist of short, common repeats that are not effective in uniquely representing the sequence as a whole (paragraph 0125) and using masks (paragraph 0063). Zhou et al. describe analyzing the complexity of the user-provided sequence and report that the sequence is insufficiently complex with too many repeats to be uniquely and/or reliably represented by a

probe set (paragraph 0126). Zhou et al. describe a method and system (vendor) enabling a number of users to share space on an array or enabling a number of users to share in ordering portions of a lot of catalog probe arrays for economical benefit (paragraphs 0005 and 0006), which represents the vendor providing at least one additional array design parameter including probe selection as well as layout parameters, as stated in instant claims 1, 5, 27, 34. Zhou et al. describe the user may select many probe array format factors such as number of probes, dimensions of probes, maximum number of probes representing one or more genes, substrate material that are received from the user (paragraph 0009) which represents receiving other selected array design parameters from the customer, as stated in instant claims 33-36. Zhou et al. describe the user may select geographic dispersion of probe sets and the user may provide some or all of the array format factors, such as substrate material or design, that are received by the user (paragraph 0009) which represents array design layout and probe parameters received from the customer, as stated in instant claims 5, 6, 34, and 35. Zhou et al. describe receiving array design layout and probe parameters from the customer and using a probe set with controls (paragraphs 0009, 0074, 0090), as stated in instant claims 7 and 36. Figure 14 shows a graphical user interface for providing options and design selections (paragraph 0039), as stated in instant claims 8 and 37. Figure 15 shows a graphical user interface for providing one or more custom probe array designs or probe set designs (layouts) (paragraphs 0010 and 0040) which represents visual display of array layout of at least one customer selected array design parameter, as stated in instant claim 9. Zhou et al. describe receiving probe set identifiers that identify potential probes and verifying probe sets of verified probes (paragraph 0007), which represents some probe selection by a vendor, as stated in instant claims 1, 27. Zhou et al. describe displaying the

custom probe array design to the user via graphical user interface and receives a user selection specifying acceptance, modification, or rejection of the design and providing accepted or modified custom probe array as well as vendor completing (i.e. shared probe array deemed complete) or customer completing (i.e. particular type of probe set ordered by user) an array design (abstract and Figure 15, 0145), as stated in instant claims 10 and 11. The user acceptance of array design represents completion of the design by the vendor, as stated in instant claims 1, 2, 22, 27, 31. The user modification of the design represents completion of the array design by the customer, as stated in instant claims 1, 3, 22, 27, 32. Zhou et al. describe providing the user with the accepted or modified custom probe array (abstract). Zhou et al. describe using arrays for genes and nucleic acids (Figure 2 #230), as stated in instant claims 4, 22, and 27. Zhou et al. describe researchers using microarrays to determine which genes are expressed in certain cells or organs, extracting biological information, and designing follow-up experiments (paragraph 0004). Zhou et al. describe the probe set identifiers may be selected by the user from a predetermined list where each item may correspond to an EST, gene, splice variant, or protein (paragraph 0009) which represents selecting at least one gene of interest and probe parameter for said gene, as stated in instant claim 27. Zhou et al. describe systems, methods, and computer program products to address these needs, such as allowing the user to select probe identifiers that may be associated with probe sets of one or more probes that are capable of detecting genes of interest, which are then correlated with data and/or products to be provided to the user (paragraph 0006), as stated in instant claim 27. Figures 7A and 10 show displaying and providing genomic data, sequence data, expression data, and various other forms of information to the user (paragraphs 0030 and 0034), as stated in instant claim 27. Zhou et al. describe

synthesizing probes on a substrate (paragraph 0090), as stated in instant claim 28. Zhou et al. describe selecting substrate material or design and synthesized probe arrays (paragraph 0010), as stated in instant claim 28. Zhou et al. describe constructing probe arrays to detect or measure one or any combination of biological information including gene expression, genotype, cells, cellular membranes, and organelles (paragraph 0007) which represents an in situ array, as stated in instant claim 41. Zhou et al. provisional (60/301,298) does not specifically state curating or curated sequence (instant claim 1, steps c) and d)) or describe all of the curating limitations in claims 42-44 and 47-49.

Markowitz et al. describe offering gene chip technology manufacturing glass microarrays with probes (0006). Markowitz et al. describe using custom gene sequences (0037), user selection and user-selected gene attributes (parameters) (0110, 0229) allowing users to specify parameters and adjust parameters (0050), sequence searching for a user-provided nucleotide sequence against a database of GenBank sequences corresponding to Affymetrix (vendor) probe sets (0249), and sequence based matching and manual data curation including detecting potential sequence data contamination (0043, 0046) which represents database searching and curating sequence data, as stated in instant claims 1, 22, 27. Markowitz et al. describe the user entering search parameters with the search completing by listing Affy fragments that match the input sequence (0253) and the Gene Set Import Utility allowing a user to create a Gene Set based on a list of Affy probe set names wherein the user-selected return attribute values are queried followed by displaying the query results after which the user can save the fragments if he/she wishes (0255, 0245) which represents completing the array design by the customer, as stated in

instant claim 3. Markowitz et al. do not describe all of the curating limitations in claims 42-44 and 47-49.

Cracauer et al. describe a high-throughput olignucleotide production system (claim 1), designing and producing detection assays for target sequences (0434), and receiving orders from a customer who enters a target sequence into a web interface, processing orders, and designing the detection assays which can be produced and shipped to customers (0435, 0539). Cracauer et al. describe a curated sequence (0484), searching databases to obtain sequence data, identify problems, and remove problem portions of the sequence (0502-0504), searching nucleic acid databases (0071, 0447, 0453, 0460), and checking for errors in target sequence and removal of artifacts associated with sequence assembly and removal of commonly repeated subsequences (0443-0444, 0470-0475, 0541, 0101, 0369, 0505, 0653) as stated in instant claims 42-44 and 47-49.

Zhou et al. state researchers are increasingly challenged to extract biologically meaningful information from the vast amounts of data generated by microarray technologies and to design follow-up experiments (0004). Cracauer et al. state attempts to analyze individuals based on a reference genome sequence will often fail (i.e. probes based on reference sequence fail to hybridize to target sequence in another individual) because the target sequence for many individuals differs from the reference sequence (0022). It would have been obvious to one of ordinary skill in the art at the time the invention was made to modify the method of Zhou et al. by sequence searching for a user-provided nucleotide sequence against a database of GenBank sequences corresponding to Affymetrix (vendor) probe sets as taught by Markowitz et al. wherein the motivation would have been to provide a common interface for multiple databases in

a relational format to support efficient exploration and analysis, as stated by Markowitz et al. (0009) in order to extract meaningful information, as stated by Zhou et al. (0004). It would have been further obvious to one of ordinary skill in the art at the time the invention was made to modify the methods of Zhou et al. and Markowitz et al. by checking for errors and removal of sequence artifacts as taught by Cracauer et al. where the motivation would have been to select appropriate target sequences that can be successfully targeted by detection assays (0442) in order to extract meaningful information (Zhou et al. 0004).

Thus, Zhou et al. in view of Markowitz et al. and Cracauer et al. make obvious the instant invention.

Applicant argues that Zhou et al. do not describe curating or removing commonly repeated subsequences in paragraphs 0005, 0010, 0063. This statement is found moot as Cracauer et al. describe curating and removing commonly repeated subsequences, as discussed in the rejection above. Applicant summarizes Zhou et al.'s paragraph 0126 and argues this cannot be the case in the instant claims as notification of at least one gene of interest is received from a customer, not merely a sequence, as in Zhou et al. This statement is found unpersuasive as Zhou et al. describe a user requesting a corresponding probe set for a specified gene sequence (0093), and receiving one or more genes from a user as well as user notations (0168 and 0169) which reasonably represents the notification limitation. Applicant summarizes the database searching and curating limitations in instant claims 1, 22, 27. Applicant summarizes Markowitz et al. and argues that Markowitz et al. do not describe array design or fabrication or probe selection. This

statement is found unpersuasive as this is a 35 USC 103 rejection such that a single reference does not need to address all the limitations in the rejected claims. It is noted that Zhou et al. describe array design and fabrication and probe selection. Applicant again argues that Zhou et al. do not describe notification of at least one gene of interest is received from a customer. This statement has already been found unpersuasive for the reasons given above. Applicant argues that the curation of Markowitz et al. is carried out to classify certain gene fragments and not for probe selection. This statement is found unpersuasive as Markowitz et al. do not need to recite all the claim limitations in a 35 USC 103 rejection, and Zhou et al. describe probe selection (i.e. 0093, 0124, 0125). Applicant argues that Zhou et al. do not receive a selected gene of interest, perform database searching for sequence data for probe selection for the at least one gene of interest, and curate the sequence data for use in probe selection obtained by the database searching after the database searching. This statement is found unpersuasive as Zhou et al. describe the following:

> Zhou et al. describe a user requesting a corresponding probe set for a specified gene sequence (0093), and receiving one or more genes from a user as well as user notations (0168 and 0169) which represents receiving from a customer, at least one array design parameter and notification of at least one gene of interest, as stated in instant claims 1, 22, 27. Zhou et al. describe accessing databases to provide researchers with associations between probe sets and gene identifiers, using Entrez search and retrieval system that provides information from various NCBI databases including nucleotide sequences, including accessing NCBI Entrez nucleotide database, and associations of a gene or probe-set identifier to products and a genomics database (0075, 0076, 0084, 0033, 0027, 0028, 0034), a user requesting a corresponding probe set for a specified gene sequence, and a database with the sequence or sequences from which the probes are designed (0093), and accessing/searching a database to obtain sequence data for probe selection for at least one gene of interest such that the correspondence may be provided to the user (0095, 0096, 0124, 0110, 0112, 0116, 0119, 0122), searching database for user provided sequence to verify existence of one or more corresponding probe sets and correlating identity of probe sets having a corresponding sequence with probe set identifiers (0124), or analyzing user provided input sequence to determine which portions should be represented by probes (0125), and databases including information relating probe set

identifiers to probe sequences (0114) which represents database searching to obtain sequence data for probe selection for at least one gene of interest.

It is noted that besides Markowitz et al. describing curating, Cracauer et al. describe a curated sequence (0484), searching databases to obtain sequence data, identify problems, and remove problem portions of the sequence (0502-0504), checking for errors in target sequence and removal of artifacts associated with sequence assembly and removal of commonly repeated subsequences (0443-0444, 0470-0475, 0541, 0101, 0369, 0505, 0653).

Applicant argues that user modification of the design does not represent completion of the array design by the customer. This statement is found unpersuasive as Zhou et al. describe displaying the custom probe array design to the user via graphical user interface, receiving a user selection specifying acceptance, modification, or rejection of the design and providing accepted or modified custom probe array as well as vendor completing (i.e. shared probe array deemed complete) or customer completing (i.e. particular type of probe set ordered by user) an array design (abstract and Figure 15, 0145, claim 1), as stated in instant claims 10 and 11. The user acceptance of array design represents completion of the design by the vendor. The user modification of the design reasonably represents completion of the array design by the customer, because the customer had the final word. Applicant argues that Applicant does not find these limitations in claims 10 and 11 of Zhou et al. This statement is found moot as instant claims 10 and 11 are referring to claims 10 and 11 of the instant application. The limitations may be found in Zhou et al.'s abstract and Figure 15. Applicant argues it appears in Zhou et al. if the user rejects and modifies a proposed custom design, the system then goes back and generates another custom design and presents it to the user to repeat the approval process, as stated in the abstract. This statement is found unpersuasive as the Zhou et al. abstract does not mention the system then

goes back and generates another custom design and presents it to the user to repeat the approval process, but rather a user selection specifying modification and then the system providing the modified custom probe array based on the probe array design and responsive to the user modification (also see claim 1 of Zhou et al.). This passage suggests the customer had the final say and completed the array design.

Applicant summarizes Cracauer et al. and argues that Cracauer et al. do not curate sequence data for probe selection. This statement is found unpersuasive as Cracauer et al. do not need to recite every limitation in the 35 USC 103 rejection. It is noted that curating activities, such as those described in instant claims 42-44 and 47-49 are described by Cracauer et al. (0443-0444, 0470-0475, 0484, 0502-0504, 0541, 0101, 0369, 0505, 0653). Applicant argues that Cracauer et al. do not describe inputting at least one user selected gene, database searching, and curating. This statement is found unpersuasive as Zhou et al. describe receiving a notification of at least one gene of interest from a customer and database searching, as already discussed above. In addition, Cracauer et al. describe searching databases to obtain sequence data, identify problems, and remove problem portions of the sequence (0502-0504). Applicant argues that combining the references is not proper. This statement is found unpersuasive as the motivational statements for reasons to combine the references have been provided in the rejection above.

Applicant's arguments are deemed unpersuasive for the reasons given above.

Conclusion

No claim is allowed.

THIS ACTION IS MADE FINAL. Applicant is reminded of the extension of time policy as set forth in 37 CFR 1.136(a).

A shortened statutory period for reply to this final action is set to expire THREE MONTHS from the mailing date of this action. In the event a first reply is filed within TWO MONTHS of the mailing date of this final action and the advisory action is not mailed until after the end of the THREE-MONTH shortened statutory period, then the shortened statutory period will expire on the date the advisory action is mailed, and any extension fee pursuant to 37 CFR 1.136(a) will be calculated from the mailing date of the advisory action. In no event, however, will the statutory period for reply expire later than SIX MONTHS from the mailing date of this final action.

Papers related to this application may be submitted to Technical Center 1600 by facsimile transmission. Papers should be faxed to Technical Center 1600 via the PTO Fax Center. The faxing of such papers must conform with the notices published in the Official Gazette, 1096 OG 30 (November 15, 1988), 1156 OG 61 (November 16, 1993), and 1157 OG 94 (December 28, 1993) (See 37 CFR §1.6(d)). The Central Fax Center number for official correspondence is (571) 273-8300.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see http://pair-direct.uspto.gov. If you have questions on access to the Private PAIR system, please contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free). If you

would like assistance from a USPTO Customer Service Representative or access to the automated information system, please call 800-786-9199 (IN USA OR CANADA) or 571-272-1000.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Carolyn Smith, whose telephone number is (571) 272-0721. The examiner can normally be reached Monday through Thursday from 8 A.M. to 6:30 P.M.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Marjorie Moran, can be reached on (571) 272-0720.

August 26, 2008

/Carolyn Smith/
Primary Examiner
AU 1631